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Figures

Replacement Sheet

line numbers edited
throughout to establish
total number of pages

Figure 1 - Nucleotide and protein sequence of *Aspergillus ochraceus* 11

alpha hydroxylase

5	tggaagtttt tacacttatt atgccggagc cgaagattc tgagtcgagg ggttggggaa	60
	caacactata agacctacaa ccaattggat ttggtgaatt tacacgggca ttatcaaaac	120
	agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg	172
	Met Pro Phe Phe Thr Gly Leu Leu Ala	
	1 5	
10	att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc	220
	Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr	
	10 15 20 25	
15	att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc	268
	Ile Val Val Leu Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser	
	30 35 40	
20	gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt	316
	Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg	
	45 50 55	
25	cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg	364
	Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg	
	60 65 70	
30	ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg	412
	Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp	
	75 80 85	
35	gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac	460
	Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn	
	90 95 100 105	
40	gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga	508
	Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Thr Asp Asp Ser His Gly	
	110 115 120	
45	tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa	556
	Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys	
	125 130 135	
50	gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg	604
	Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro	
	140 145 150	
55	atc tcg cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat	652
	Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp	
	155 160 165	
60	cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc	700
	Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val	
	170 175 180 185	
65	gcc cgg atg tcg aca aga gtg ttc ctt gcc gag gaa atg tgc aat aac	748
	Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Glu Met Cys Asn Asn	
	190 195 200	
70	cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt	796
	Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly	
	205 210 215	
75	gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta	844
	Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val	
	220 225 230	
80	cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tcg ctg cga cgc	892
	His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Arg Ser Leu Arg Arg	
	235 240 245	
85	tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag	940
	Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys	
	250 255 260 265	

Sequence moved
to page 2 of 25
for continuity in
formatting

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insert

"figure 1, continued"

5	ggg acc acg gac gag cag ggc aag ccc ctt atg ttt gat gat tcc atc Gly Thr Thr Asp 270 Gln Gly Lys Pro 275 Leu Met Phe Asp Asp Ser Ile 280	988
10	gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag Glu Trp Phe 285 Glu Arg Glu Leu Gly 290 Pro Asn His Asp Ala Val Leu Lys 295	1036
15	cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc Gln Val Thr 300 Leu Ser Ile Val Ala Ile His Thr Thr Ser Asp Leu Leu 310	1084
20	ttg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca Leu Gln Ala Met Ser Asp 315 Leu Ala Gln Asn Pro Lys Val Leu Gln Ala 320	1132
25	gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag Val Arg Glu Glu Val 335 Arg Val Leu Ser Thr Glu Gly Leu Ser Lys 340	1180
30	gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc Val Ser Leu His 350 Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser 360	1228
35	cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr 375	1276
40	aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga Asn Asp Ile Lys Leu Lys Ser 380 Gly Phe Val Ile Lys Lys Gly Thr Arg 390	1324
45	gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp 405	1372
50	cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc Pro Leu Gln Tyr Asp 410 Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro 425	1420
55	ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met 430	1468
60	gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser 445	1516
65	aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp 460	1564
70	cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act Arg Leu Pro Asp Gly Phe Lys 475 Pro Gln Pro Leu Asn Ile Gly Met Thr 485	1612
75	tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala 490	1660
80	gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtcctgat Glu Ile Asp Met Ala Ser Leu Thr Val 510	1710
85	gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat aaaaaa	1770 1776

line numbers changed to address additional lines
originally on page 1 of 25.

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**Figure 2 - Nucleotide and protein sequence of human
oxidoreductase**

5	atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg Met Gly Asp Ser His Val Asp Thr Ser Thr Val Ser Glu Ala Val	48
	1 5 10 15	
10	gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser	96
	20 25 30	
15	ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys	144
	35 40 45	
20	gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val	192
	50 55 60	
25	aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile	240
	65 70 75 80	
30	atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn	288
	85 90 95	
35	cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala	336
	100 105 110	
40	gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile	384
	115 120 125	
45	gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp	432
	130 135 140	
50	ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp	480
	145 150 155 160	
55	gtg gat ctc tct ggg gtc aag ttc gcg gtg ttt ggt ctt ggg aac aag Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys	528
	165 170 175	
60	acc tac gag cac ttc aat gcc atg ggc aag tac gtg gac aag cgg ctg Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu	576
	180 185 190	
65	gag cag ctc ggc gcc cag cgc atc ttt gag ctg ggg ttg ggc gac gac Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp	624
	195 200 205	
70	gat ggg aac ttg gag gag gac ttc atc acc tgg cga gag cag ttc tgg Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp	672
	210 215 220	
75	ccg gcc gtg tgt gaa cac ttt ggg gtg gaa gcc act ggc gag gag tcc Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser	720
	225 230 235 240	
80	agc att cgc cag tac gag ctt gtg gtc cac acc gac ata gat gcg gcc Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala	768
	245 250 255	
85	aag gtg tac atg ggg gag atg ggc cgg ctg aag agc tac gag aac cag Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln	816
	260 265 270	
90	aag ccc ccc ttt gat gcc aag aat cgg ttc ctg gct gca gtc acc acc Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr	864
	275 280 285	
95	aac cgg aag ctg aac cag gga acc gag cgc cac ctc atg cac ctg gaa	912

↓ Sequence moved
to improve
continuity

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← insert

"Figure 2, continued"

	Asn	Arg	Lys	Leu	Asn	Gln	Gly	Thr	Glu	Arg	His	Leu	Met	His	Leu	Glu	
	290						295					300					
5	ttg	gac	atc	tcg	gac	tcc	aaa	atc	agg	tat	gaa	tct	ggg	gac	cac	gtg	960
	Leu	Asp	Ile	Ser	Asp	Ser	Lys	Ile	Arg	Tyr	Glu	Ser	Gly	Asp	His	Val	
	305					310					315					320	
10	gct	gtg	tac	cca	gcc	aac	gac	tct	gct	ctc	gtc	aac	cag	ctg	ggc	aaa	1008
	Ala	Val	Tyr	Pro	Ala	Asn	Asp	Ser	Ala	Leu	Val	Asn	Gln	Leu	Gly	Lys	
					325					330					335		
15	atc	ctg	ggt	gcc	gac	ctg	gac	gtc	gtc	atg	tcc	ctg	aac	aac	ctg	gat	1056
	Ile	Leu	Gly	Ser	Ala	Asp	Leu	Asp	Val	Val	Met	Ser	Leu	Asn	Asn	Leu	
				340					345					350			
20	gag	gag	tcc	aac	aag	aag	cac	cca	ttc	ccg	tgc	cct	acg	tcc	tac	cgc	1104
	Glu	Glu	Ser	Asn	Lys	Lys	His	Pro	Phe	Pro	Cys	Pro	Thr	Ser	Tyr	Arg	
			355					360					365				
25	acg	gcc	ctc	acc	tac	tac	ctg	gac	atc	acc	aac	ccg	ccg	cgt	acc	aac	1152
	Thr	Ala	Leu	Thr	Tyr	Tyr	Leu	Asp	Ile	Thr	Asn	Pro	Pro	Arg	Thr	Asn	
		370					375					380					
30	gtg	ctg	tac	gag	ctg	ggc	cag	tac	gcc	tcg	gag	ccc	tcg	gag	cag	gag	1200
	Val	Leu	Tyr	Glu	Leu	Ala	Gln	Tyr	Ala	Ser	Glu	Pro	Ser	Glu	Gln	Glu	
	385					390					395				400		
35	ctg	ctg	cgc	aag	atg	gcc	tcc	tcc	ggc	gag	ggc	aag	gag	ctg	tac		1248
	Leu	Leu	Arg	Lys	Met	Ala	Ser	Ser	Ser	Gly	Glu	Gly	Lys	Glu	Leu	Tyr	
				405						410				415			
40	ctg	agc	tgg	gtg	gtg	gag	gcc	cgg	agg	cac	atc	ctg	gcc	atc	ctg	cag	1296
	Leu	Ser	Trp	Val	Val	Glu	Ala	Arg	Arg	His	Ile	Leu	Ala	Ile	Leu	Gln	
			420					425					430				
45	gac	tgc	ccg	tcc	ctg	cgg	ccc	ccc	atc	gac	cac	ctg	tgt	gag	ctg	ctg	1344
	Asp	Cys	Pro	Ser	Leu	Arg	Pro	Pro	Ile	Asp	His	Leu	Cys	Glu	Leu	Leu	
			435				440					445					
50	ccg	cgc	ctg	cag	gcc	cgc	tac	tac	tcc	atc	gcc	tca	tcc	tcc	aag	gtc	1392
	Pro	Arg	Leu	Gln	Ala	Arg	Tyr	Tyr	Ser	Ile	Ala	Ser	Ser	Ser	Lys	Val	
		450				455						460					
55	cac	ccc	aac	tct	gtg	cac	atc	tgt	gcg	gtg	gtt	gtg	gag	tac	gag	acc	1440
	His	Pro	Asn	Ser	Val	His	Ile	Cys	Ala	Val	Val	Val	Val	Glu	Tyr	Glu	
	465				470					475				480			
60	aag	gcc	ggc	cgc	atc	aac	aag	ggc	gtg	gcc	acc	aac	tgg	ctg	cgg	gcc	1488
	Lys	Ala	Gly	Arg	Ile	Asn	Lys	Gly	Val	Ala	Thr	Asn	Trp	Leu	Arg	Ala	
			485					490						495			
65	aag	gag	cct	gcc	ggg	gag	aac	ggc	ggc	cgt	gcg	ctg	gtg	ccc	atg	ttc	1536
	Lys	Glu	Pro	Ala	Gly	Glu	Asn	Gly	Gly	Arg	Ala	Leu	Val	Pro	Met	Phe	
			500					505					510				
70	gtg	cgc	aag	tcc	cag	ttc	cgc	ctg	ccc	ttc	aag	gcc	acc	acg	cct	gtc	1584
	Val	Arg	Lys	Ser	Gln	Phe	Arg	Leu	Pro	Phe	Lys	Ala	Thr	Thr	Pro	Val	
		515						520				525					
75	atc	atg	gtg	ggc	ccc	ggc	acc	ggg	gtg	gca	ccc	ttc	ata	ggc	ttc	atc	1632
	Ile	Met	Val	Gly	Pro	Gly	Thr	Gly	Val	Ala	Pro	Phe	Ile	Gly	Phe	Ile	
		530				535						540					
80	cag	gag	cgg	gcc	tgg	ctg	cga	cag	cag	ggc	aag	gag	gtg	ggg	gag	acg	1680
	Gln	Glu	Arg	Ala	Trp	Leu	Arg	Gln	Gln	Gly	Lys	Glu	Val	Gly	Glu	Thr	
	545				550					555					560		
85	ctg	ctg	tac	tac	ggc	tgc	cgc	cgc	tcg	gat	gag	gac	tac	ctg	tac	cgg	1728
	Leu	Leu	Tyr	Tyr	Gly	Cys	Arg	Arg	Ser	Asp	Glu	Asp	Tyr	Leu	Tyr	Arg	
				565					570					575			
90	gag	gag	ctg	gcg	cag	ttc	cac	agg	gac	ggt	gcg	ctc	acc	cag	ctc	aac	1776
	Glu	Glu	Leu	Ala	Gln	Phe	His	Arg	Asp	Gly	Ala	Leu	Thr	Gln	Leu	Asn	
				580				585					590				
95	gtg	gcc	ttc	tcc	cgg	gag	cag	tcc	cac	aag	gtc	tac	gtc	cag	cac	ctg	1824
	Val	Ala	Phe	Ser	Arg	Glu	Gln	Ser	His	Lys	Val	Tyr	Val	Gln	His	Leu	
		595				600						605					
100	cta	aag	caa	gac	cga	gag	cac	ctg	tgg	aag	ttg	atc	gaa	ggc	ggt	gcc	1872
	Leu	Lys	Gln	Asp	Arg	Glu	His	Leu	Trp	Lys	Leu	Ile	Glu	Gly	Gly	Ala	

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	610	615	620	
5	cac atc tac gtc tgt ggg gat gca cgg aac atg gcc agg gat gtg cag His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln 625 630 635 640	1920		
10	aac acc ttc tac gac atc gtg gct gag ctc ggg gcc atg gag cac gcg Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala 645 650 655	1968		
15	cag gcg gtg gac tac atc aag aaa ctg atg acc aag ggc cgc tac tcc Gln Ala Val Asp Tyr Ile Lys Lys Leu Met Thr Lys Gly Arg Tyr Ser 660 665 670	2016		
	ctg gac gtg tgg agc Leu Asp Val Trp Ser 675	2031		

← insert

Figure 2, continued

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Figure 3 - Nucleotide and protein sequence of *Aspergillus ochraceus oxidoreductase*

5	cttatttcgt ttaggaagag caccggcttc ggtgtccttc cttaccctct tattcttctc	60
	cttctgactc cctttttgtt attgatcgcc catctcgggt aacatttggg atatctttcc	120
	ctctccccc cccgccccga ccttccttat cttctcctcc cgtccagcat ttagctcgcc	180
	atcgaattcg caattccttc ctcgtgactc ttcacgctg agcgtcctca tc atg gcg	238
	Met Ala	
10	caa ctc gat act ctc gat ttg gtc gtc ctg gtg gcg ctc ttg gtg ggt	286
	Gln Leu Asp Thr Leu Asp Leu Val Val Leu Val Ala Leu Leu Val Gly	
	5 10 15	
15	agc gtg gcc tac ttc acc aag ggc acc tac tgg gcc gtc gcc aaa gac	334
	Ser Val Ala Tyr Phe Thr Lys Gly Thr Tyr Trp Ala Val Ala Lys Asp	
	20 25 30	
20	cct tat gcc tcg gct ggt ccg gcg atg aat gga ggc gcc aag gcc ggc	382
	Pro Tyr Ala Ser Ala Gly Pro Ala Met Asn Gly Gly Ala Lys Ala Gly	
	35 40 45 50	
25	aag act cgc gac att gtt cag aaa atg gac gaa act ggc aaa aac tgt	430
	Lys Thr Arg Asp Ile Val Gln Lys Met Asp Glu Thr Gly Lys Asn Cys	
	55 60 65	
30	gtg att ttc tac ggc tcg caa acc ggt acc gct gag gac tac gcg tcc	478
	Val Ile Phe Thr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala Ser	
	70 75 80	
35	aga ctg gcc aag gaa ggc tcc cag cga ttc ggt ctc aag acc atg gtg	526
	Arg Leu Ala Lys Glu Gly Ser Gln Arg Phe Gly Leu Lys Thr Met Val	
	85 90 95	
40	gcc gat ctg gag gac tac gac tac gaa aac ctg gaa aag ttc ccc gag	574
	Ala Asp Leu Glu Asp Tyr Asp Tyr Glu Asn Leu Glu Lys Phe Pro Glu	
	100 105 110	
45	gac aag gtt gtt ttc ttc gtt ctg gcc act tat ggc gag ggt gaa ccc	622
	Asp Lys Val Val Phe Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu Pro	
	115 120 125 130	
50	acg gat aat gcg gtt gaa ttc tac cag ttc gtc acg ggc gaa gat gct	670
	Thr Asp Asn Ala Val Glu Phe Tyr Gln Phe Val Thr Gly Glu Asp Ala	
	135 140 145	
55	gct ttc gag agc ggc gct acc gcc gac gat aag cct ctg tct tct ctc	718
	Ala Phe Glu Ser Gly Ala Thr Ala Asp Asp Lys Pro Leu Ser Ser Leu	
	150 155 160	
60	aag tat gtc acg ttt ggt ctg ggt aac aac acc tat gag cac tac aac	766
	Lys Tyr Val Thr Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn	
	165 170 175	
65	gct atg gtt cgc aat gtg gac gcc gct ctc aca aag ttc ggc gcc caa	814
	Ala Met Val Arg Asn Val Asp Ala Ala Leu Thr Lys Phe Gly Ala Gln	
	180 185 190	
70	cgc att ggc tct gct ggt gag ggt gac gac ggc gct ggt aca atg gaa	862
	Arg Ile Gly Ser Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu	
	195 200 205 210	
75	gag gat ttc ctg gcc tgg aag gaa ccc atg tgg gct gcc ctt tct gag	910
	Glu Asp Phe Leu Ala Trp Lys Glu Pro Met Trp Ala Ala Leu Ser Glu	
	215 220 225	
80	gcg atg aac ctg caa gag cgc gat gcg gtc tac gag ccg gtc ttc aat	958
	Ala Met Asn Leu Gln Glu Arg Asp Ala Val Tyr Glu Pro Val Phe Asn	
	230 235 240	
85	gtc acc gag gac gag tcc ctg agc ccc gaa gat gag aac gtt tac ctc	1006
	Val Thr Glu Asp Glu Ser Leu Ser Pro Glu Asp Glu Asn Val Tyr Leu	
	245 250 255	
90	ggt gag ccc act caa ggt cat ctc caa ggc gag ccc aag ggc ccg tac	1054
	Gly Glu Pro Thr Gln Gly His Leu Gln Gly Glu Pro Lys Gly Pro Tyr	

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← Insert

"Figure 3, continued"

	260	265	270	
5	tct gcg cac aac ccg ttc atc gct ccc atc tcc gaa tct cgt gaa ctg Ser Ala His Asn Pro Phe Ile Ala Pro Ile Ser Glu Ser Arg Glu Leu 275 280 285 290	1102		
10	ttc aac gtc aag gac cgc aac tgt ctg cac atg gaa atc agc atc gcc Phe Asn Val Lys Asp Arg Asn Cys Leu His Met Glu Ile Ser Ile Ala 295 300 305	1150		
15	ggg agc aac ctc act tac cag act ggt gac cac atc gct gtt tgg ccc Gly Ser Asn Leu Thr Tyr Gln Thr Gly Asp His Ile Ala Val Trp Pro 310 315 320	1198		
20	acc aac gcc ggt tcc gag gtc gat cgg ttc ctg cag gct ttt ggt ctc Thr Asn Ala Gly Ser Glu Val Asp Arg Phe Leu Gln Ala Phe Gly Leu 325 330 335	1246		
25	gaa gga aag cgc cac tcc gtc atc aac att aag ggt atc gat gtg acc Glu Gly Lys Arg His Ser Val Ile Asn Ile Lys Gly Ile Asp Val Thr 340 345 350	1294		
30	gct aag gtt ccg att ccc act cct acg acc tat gac gcc gca gtt cgc Ala Lys Val Pro Ile Pro Thr Pro Thr Thr Tyr Asp Ala Ala Val Arg 355 360 365 370	1342		
35	tac tac ctg gaa gtc tgt gcc ccc gtt tcc cgt cag ttt gtc tcg act Tyr Tyr Leu Glu Val Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr 375 380 385	1390		
40	ctc gct gcc ttt gcc cct gat gaa gcg acc aag gcg gag atc gtt cgt Leu Ala Ala Phe Ala Pro Asp Glu Ala Thr Lys Ala Glu Ile Val Arg 390 395 400	1438		
45	ttg ggt ggc gac aag gac tat ttc cat gag aag att acc aac cga tgc Leu Gly Gly Asp Lys Asp Tyr Phe His Glu Lys Ile Thr Asn Arg Cys 405 410 415	1486		
50	ttc aac atc gct cag gct ctc cag agc atc acg tcc aag cct ttc acc Phe Asn Ile Ala Gln Ala Leu Gln Ser Ile Thr Ser Lys Pro Phe Thr 420 425 430	1534		
55	gcc gtc ccg ttc tcc ctg ctt atc gaa ggt atc acc aag ctt cag ccc Ala Val Pro Phe Ser Leu Leu Ile Glu Gly Ile Thr Lys Leu Gln Pro 435 440 445 450	1582		
60	cgt tac tac tcg atc tcc tcg tct tcc ctg gtt cag aag gac aag att Arg Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Lys Asp Lys Ile 455 460 465	1630		
65	agc att acc gcc gtt gtg gag tcg gtt cgc ttg cct ggt gag gaa cac Ser Ile Thr Ala Val Val Glu Ser Val Arg Leu Pro Gly Glu Glu His 470 475 480	1678		
70	att gtc aag ggt gtg acc acg aac tat ctt ctc gcg ctc aag gaa aag Ile Val Lys Gly Val Thr Thr Asn Tyr Leu Leu Ala Leu Lys Glu Lys 485 490 495	1726		
75	caa aac ggc gag cct tcc cct gac ccg cac ggc ttg act tac tct atc Gln Asn Gly Glu Pro Ser Pro Asp Pro His Gly Leu Thr Tyr Ser Ile 500 505 510	1774		
80	act gga ccc cgt aac aag tac gat ggc atc cat gtc ccc gtt cac gtc Thr Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val 515 520 525 530	1822		
	cgc cac tcg aac ttc aaa ttg ccc tcg gat ccc tcg cga cct gtg atc Arg His Ser Asn Phe Lys Leu Pro Ser Asp Pro Ser Arg Pro Val Ile 535 540 545	1870		
	atg gtt gga ccc ggt act ggt gtt gct cct ttc cgt ggg ttt atc cag Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Ile Gln 550 555 560	1918		
	gag cgt gct gcc ttg gcc gcg aag ggc gag aag gtc gga act acc ttg Glu Arg Ala Ala Leu Ala Ala Lys Gly Glu Lys Val Gly Thr Thr Leu 565 570 575	1966		
	ctt ttc ttc ggc tgc cgt aag tcc gac gaa gat ttc ttg tac aag gat Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe Leu Tyr Lys Asp 580 585 590	2014		

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Figure 3, continued

5	gaa tgg aag act ttt cag gag cag ctt ggc gac tcg ctc aag atc atc Glu Trp Lys Thr Phe Gln Glu Gln Leu Gly Asp Ser Leu Lys Ile Ile 595 600 605 610	2062
	act gcc ttc tct cgt gaa tcg gct gag aaa gtc tac gtc cag cac agg Thr Ala Phe Ser Arg Glu Ser Ala Glu Lys Val Tyr Val Gln His Arg 615 620 625	2110
10	ctg cgt gag cat gcc gag ctg gtc agt gac ctg ctg aag cag aaa gcc Leu Arg Glu His Ala Glu Leu Val Ser Asp Leu Leu Lys Gln Lys Ala 630 635 640	2158
15	act ttc tat gtt tgc ggt gac gct gcc aac atg gcc cgt gaa gtc aac Thr Phe Tyr Val Cys Gly Asp Ala Ala Asn Met Ala Arg Glu Val Asn 645 650 655	2206
20	ctc gtg ctt ggg caa atc att gcc aag cag cgc ggt ctc cct gcc gag Leu Val Leu Gly Gln Ile Ile Ala Lys Gln Arg Gly Leu Pro Ala Glu 660 665 670	2254
25	aag ggc gag gag atg gtg aag cac atg cgc agc agc ggc agc tac cag Lys Gly Glu Glu Met Val Lys His Met Arg Ser Ser Gly Ser Tyr Gln 675 680 685 690	2302
	gac gat gtc tgg tcc taa aa Asp Asp Val Trp Ser *	2322
	695	

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**Figure 4 - Amino acid homology alignment of *A. ochraceus* 11
alpha hydroxylase with the top 10 BLAST hits from GenBank**

	CAA75565	1	---MANHSSSYHEFYKDHSHTVLRLMSEKPVILPSLIIGTCAVLLCIQWLK--PQPLIM
	CAB91316	1	-----MERLDIKSIIDPSATPFYSYLVTAFLAVVVVSLQGPRF-PKNIKH
5	CAB56503	1	-----LLFCFILSKTTKKFGQNSQYS-NHDELP
	AAB94588	1	-----MVMEHNNHTPFYIYFITSILFIFFVFFKLQVRS--DSKTS-STCKLP
	pMON45624	1	-----MPFFTGLLAIYHSLILDNPVQTLSTIVVLAAYLA-LATLQ--PSDLPE
	CAA75566	1	-----MSIFNMITSYAGSOLLPPFYIAIFVFTLVFWAIRFWLELRK-GSVVPL
10	AAD34552	1	---MTVDALTQPHLLSLAWNDTQOHGSWFAPLVTSAGLLCLLLLCSSGR--RSDLPV
	CAA75567	1	-----
	CAA76703	1	MSKSNMNSTSHETLFQQLVLGLDRMPLMDVHVLIVAFGAWLCSVIHVLSSSSTVKVP
	CAA57874	1	-----
	CAA91268	1	-----MALLILSLVISIFTFFIYIILARRERKRLREKIGLSGPEPH
15			
	CAA75565	56	VNGRKFGELSNVRAIRDITFGAROLLEKCLKMSPDKPFRIGDVGEHLILPKYAYEVVN
	CAB91316	45	LNKKGPLEFSDTRPKKEVYGSSEOMLANWFKANPNKPCRVHSEFGEALVUPPRMANETIN
	CAB56503	28	PGEPQIPILGNARQLSGGH-THHIDRLAKKYGPLMHLN-IGEVSTIVASSPQIABETFR
	AAB94588	45	PGERTLPLIGNIHQIVGSLPVHYVTKNLADKYGPLMHLN-IGEVSNLIVTSEMAQETMK
20	pMON45624	46	LNKAKPFETNRRVHEFVENSASLLARGLRHGHEPYRLSEWGSLLIVPPECADLELN
	CAA75566	48	ANEPD-SLFGTGRTRRSVKLSRRTIAKERSLFPNEPFRITDVGWVLIILPDRFADELRN
	AAD34552	56	FNEKIWWELTTMAKRDIDANAPSWIESWFSQN-DKPIRFIVSGGYCTIHSMADEFEK
	CAA75567	1	-----
25	CAA76703	61	VVGYSVFEPTWLLRLRVWEGGSILGQSYNKFKDSIFQVRKLGTDIVITPPNYIDEVRK
	CAA57874	1	-----
	CAA91268	43	WFLGNLQTAERZELGDDANWFNLFHEQYGETFGIY-YGSQMNIVISNEKDIKEVFI
30			
	CAA75565	116	NEKLSSTMAA--FKWFYAHLFGFEG--FREGTNESHKILMARHOLT--HQLTLVTGAVS
	CAB91316	105	DDRUSETRWT--YKAFEGHLPFGFEG--FGEASRESHIVQEVIMRDLT--RYLNKVTETPLA
	CAB56503	86	THDILADRPNLESFRIVSYFSDMVVSYPGNYWQRLKISMELLSQLSQQSFRSIRE
	AAB94588	104	THDILASDRP-DFVLSRIVSYVNGSGIVFSQHGDYVWQRLKICTVELTAKRVQSFERSIRE
	pMON45624	106	DPRDDETPT--TDDSHGYIFCFDA----LN-ADPNLTNVTKYLT--KALNKLTAFTIS
	CAA75566	107	DPRUSESKAA--MQDNHAGIPGFET--VALVGREDQLKQVARKQLT--RHLSAVIEPLS
35	AAD34552	115	MKELCMYKFLG--TDFHSHLPFGFDG--FKEVTRDAHLTKVMNQFO--TQAPKYVKPLA
	CAA75567	1	-----
	CAA76703	121	LS----QDKTRSVEPFINDFACQYT--RGMVFLQSDLQNRVIOQLT--PKLVSETKVEK
	CAA57874	1	-----
40	CAA91268	102	KNFSNLSDRS--VPSIYEANQLTASLLMNSYSSGWNHTRSAIPIFS-TGKKAKQETIN
45			
	CAA75565	170	ECALVVKDYVTDSP--EWHDTAKDANKLMARITSRVFECKDEKCRNPQNLRT-STVA
	CAB91316	159	QETSMAMEANLPKAANGESTINRSKILPIVARISSRVFEGEELCRNEWLKVT-QQYT
	CAB56503	146	EVVLNFIKSTG---SKEG-TRINLSKEHSLDIYGIITRAAHGEKNKNTBFFIRLDQLTK
	AAB94588	163	EVVAELVKKTAATAASEEGGSIFNTQSTYSSTFGIAAFAAGCKKSRYQVEFISNMHKQLM
	pMON45624	156	HASIAKAVLGDDP--DWRETPARDLQVARESTRVFTGCEBMQNDWQTS-SQVA
	CAA75566	161	RSTLAVSLNFGETT--EKRAIRKPAILDILARISSRYLGDOLCRNEAWLKIT-KTYT
	AAD34552	169	NEASGIITDFGDSN--EWHTVPMYNQCLDMTRTVTFIMVGSRLAHNEBWLDA-KHHA
	CAA75567	17	MKTSFRWPRTS-----KSSVSVDMLRTVALLSGRAFVGLFLCRDEGWLQAS-IGYT
50	CAA76703	173	ELDYALTKEMPDMKNDKAVVDSSIMVRLISRTSRVFLGPEHCRNQEWLTTT-AEVS
	CAA57874	1	-----
	CAA91268	159	SKVDLFLDILREKAS--SGQKWDIYDDFQGLTLDVIGKCAPIIDSNCQRDRNDVIFYHPVT
55			
	CAA75565	227	VIAFRAVEELRLWF-SWLRPVVQWFHCTQSRALVQARDLINPLEER-FREEN--AEA
	CAB91316	218	LDGFGAAEDRLWF-AALRPVHWHTFESCORARADVVARSTLDEVLEK-RPOEK--AAN
	CAB56503	202	AVAEPNIADFPSSL-KFLQLSTSKYKIEIKHQFDVIVETILKGHKETINKPLS--QEN
	AAB94588	223	PLGGFSVADLYPSS-RVFQMGATG-KLEKVHRTVDVLQDIIDEHK--NNRNS--SEE
	pMON45624	213	ALAFGVGDKLRIYF-RMTRPLVHWFHSCWBEERSLRRCQILTEYTHK-RKSLK--GTT
60	CAA75566	218	TNFTASTNLRMFF-RSERPLAHWFIECRKLHQERKDAICHTPLEER-RFELE--RAA
	AAD34552	226	VTMAIQARQLRLWF-VILRPLVHWLEPQGAQLRAQVRRARQLDPIIQE-RRABF--DAC
	CAA75567	70	MQCVSIRDQLFTWS-FVLRPLIGFELFSVRSVRRHLRFAABITAPLHSQALQDEKQHRAD
	CAA76703	232	ESLPITGFIIRVVF-HILRFTAPLHSYRTLRLNVSSSGRVIGDIR--SQO-----
	CAA57874	1	-----MA-PMLRPLVYRFEERARLDQWTKERKVMASIRE--FOE--GGN
65	CAA91268	217	SKITINNFTYFHSSSPGTFHFLESTLQIHTTGCRNSTCQRTVKQVGFQDKAKFCSDYE

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"Figure 4, continued"

5 CAA75565 283 ERTGEKV--TYNFAEFLDDLAREK--EVGVYPACAOQLSLVA--LHSTIDFFTOVMFDI
CAB91316 274 ---GGKA-EHDAEAEFERTA--K--SKYYPAAAOQLVLSVE--LHTTSDLTCQVMFNL
CAB56503 259 G--EKKE-DLVEVLNLIQRRNDFE--HPLGKKNKALIFNHFSAQTETSTTDWAMCEN
AAB94588 276 R--EAVE-DLVEVLKFKQKES--E--FRLTIDNKKALIQDFIGGGTSSSVVWEGMSL
pMON45624 269 DEQCKPL-MFDRSEDFEREL----EPNHDAVVKOVLSTVA--LHTTSDLTQAMSDI
CAA75566 274 IAACQPLPVFHAHDWSEQEAEEAGTASSEFVIFOLTLSLA--LHTTYDLTQOTMIDI
AAD34552 282 RAKGLEPPRYVSTQMFEDTAK----EKWYLAAGAQLAMDFAE--LYGTSDLTIGELVDI
CAA75567 129 TLLDQTEGRGTFISALLRHLP--EELRTPEQVGIDOMLVSAF--LHTTMAITKVWEL
CAA76703 282 ---CDGN---EILSAMRDAATGEE-KQIDNIAORMILSLAS--LHTTAMTTHAMYDL
10 CAA57874 44 ---LEDPTMLDHLNCRNEHIA---DDVELQLHOMLIAVE--TVTFSSSTQATYDL
CAA91268 277 RRRGEGSDSVLEKLLNREDDKS-KPMTKQENIENCFELLAGYETTATITYCSYL

15 CAA75565 338 AQNPETIEPLREETIAVLCKQG-----KSNLSLYNLKLMDSVHKESQRLK-E-----
CAB91316 324 KNPETIEPLREEMIQVSEGC-----KKTSLYNLKLMDSVHKESQRLK-E-----
CAB56503 314 IKNPVMKKACEEVKKVFNEECN-----VDETKHOLKLYLQAVIKETILRLH-E-----
AAB94588 329 IKNPVMPEAQAEVRRVYDSKCY-----VDETKHOLLYLKSITKEIMRLH-E-----
pMON45624 321 AQNKVLCAREEVVRVLTSTG-----LSKVSITHSLKLMDSVHKESQRLK-E-----
CAA75566 332 GRHPYIEPLRQEVVOLLREE-----KKTTLFKMLKLMDSVHKESQRLK-E-----
AAD34552 336 VRRHMLLEPLRDEIRTVLQGG-----WTFASLYKLMKLMDSVHKESQRLK-E-----
CAA75567 186 VRRPYIEPLRTEMQDVFGLPDAVSPDICINNEALSRLHKLDSSTIREVORWC-E-----
CAA76703 333 CACPYIEPLRDEVKSVVGASE-----ADTALNRRHKLDSVHKESQRLK-E-----
CAA57874 96 VRRPYITLREEVESVPRDPNGN-----FIRDSIVAKDKLDSVHKESQRLK-E-----
25 CAA91268 336 SYENVCKLYEETMEAKENG-----LTYDSHNMRYLLCVYKEELRPFY-E-----

30 CAA75565 384 -----IAIASMRFFTHNVKLSQGVILPNKLTLSAHQHW-----LPSVYKE
CAB91316 370 -----TGVASMRFYAEKDLTSDCTTFPKGCFVAUSAHDW-----NSEVYKE
CAB56503 361 -----PVPLLPRECREQCKHK-CYTHFSKSRVIVNVAWAGR-----LBNYVIE
AAB94588 376 -----PVPLLPVVSRERCQIN-CYTHFSKTRIIINVAWAGR-----NPKYVIE
pMON45624 367 -----TLLGSRRFOATNDIKKSCFVHKKCTPWWIDSTHW-----NPSVYIE
CAA75566 378 -----GSIVTMRREVTEHTLSSCLTEKKCTRLNVNDRID-----DPKIYDN
AAD34552 382 -----VECATMPSYALQDVFISNCTTFPKGELVAVADRMS-----NPSVYIE
CAA75567 238 -----STFVTPSRVMKSMTLNCKIKFORGTSAFPAHANHMSEETPTFSPEFSSE
CAA76703 379 -----VFLITFNFYHQSMTLSDCTNIFSGCTRIAPVSHAKLQ-----DSAHVPG
CAA57874 152 KNYKLCESLTGHSNIPTRTIADKLPDCTFVPKCTRIEINTCSLHK-----DHKLVEN
CAA91268 382 -----PHFSFTRRLCREDLTIR-CQFYPKCAITVCLFHTVHR-----NPNVADS

40 CAA75565 427 ELK-----FDGYRFFNMREP--GNEKAQLVSATPHMGFGYGLHACPGRFFASSEIKI
CAB91316 413 AEK-----VDCRRFLRMRETPGACKENVAQLVSTAPSHLGFCHCHACPGRFFAANEIKI
CAB56503 404 BEK-----FNPDRFLES-----S---VDFKGNSEFYLFPGGRRICPCGITPALANIEL
AAB94588 419 TES-----FKPBRFLNS-----S---IDFRGIDFELIFPGGRRICPCGITPAIPNIEL
pMON45624 410 ELQ-----VDGYRYFNKRQTP--CEDKNALLVSTISANHMFGFGCHVACPGRFFASNEIKI
CAA75566 421 BEV-----VNFYRYFYDMRSEA--GRDHGAQLVSTGSNMGFGFGCHVACPGRFFAANEIKI
AAD34552 425 BAK-----YLPYFYMRUREDP--BAFSAQLENNGDHIGEGWHFACPGRFFASKEIKI
CAA75567 289 FBNPSPRIEDGFRYLNLSIK--CGSQHQAATGPLYLTENNCKHACPGRFFAISEIKI
CAA76703 423 PTP--PTFEDGFRYSKIRSDS--NYAQKYLFSMADSSNMAFGYCKYACPGRFFASNEIKI
CAA57874 205 PEQ-----FDSLRFHKWKAP--GNEKRYMYSSSGTDLSSGCFRCHACPGRYLSAINIKI
50 CAA91268 425 PBE-----SHPRFENWE-----E-----KSSSLKWTFEGVCPFYVCMRFEMSEFT

55 CAA75565 480 AISHILLRYDERPV-----EGSSMEPRKYGLNNANETAKLSVRRK-EEIAI-----
CAB91316 468 AVHLLLYVWRLP-----EGSDPKIRTFESMGVDLSLKYVNGRO-PEIEL-----
CAB56503 449 PAQLLYHEDWLPNKMKNELDMTE-SNGTLRQNDLCLIPITR-----LP-----
AAB94588 464 PAQLLYHEDWLPNKMKNELDMTE-SNGTLRQNDLCLIPITR-----LP-----
pMON45624 463 ACHITLLYVWRLP-----DGFKPOLNIGHTYLAENTRLRTRPR-ABIDMASLTV
CAA75566 474 ACHITLLYVWRLP-----PDTEKPDTRGHIASSSVTDLIRRESVBLDEAI--
AAD34552 478 MAYLLRYDWRVYV-----PDEPLQYRHSFVRIHETTLMMRRFD-EDIRLPGSL
CAA75567 347 ILIELLAKYDERLE-----DGKPGPELMRVCTETRLDTKAGLEMRFR-----
CAA76703 479 TLAILLLOFEERLP-----DGKGRPRNITIDSDMIPDLARLQVRRKS-----LRDE-----
CAA57874 258 IMAELLRYDTRLP-----DGLSRPKNIEFVLASLNACANA-----
CAA91268 468 TVVKLLDTFELNDF-----EGEADLIPDCNGVIMEFNDPVRLHLKPRN-----

60 CAA75565 (SEQ ID NO: 27)
CAB91316 (SEQ ID NO: 28)
CAB56503 (SEQ ID NO: 29)
AAB94588 (SEQ ID NO: 30)
pMON45624 (SEQ ID NO: 02)
CAA75566 (SEQ ID NO: 31)
AAD34552 (SEQ ID NO: 32)
CAA75567 (SEQ ID NO: 33)
CAA76703 (SEQ ID NO: 34)
CAA57874 (SEQ ID NO: 35)
CAA91268 (SEQ ID NO: 36)

65 CAA75565 (SEQ ID NO: 27)
CAB91316 (SEQ ID NO: 28)
CAB56503 (SEQ ID NO: 29)
AAB94588 (SEQ ID NO: 30)
pMON45624 (SEQ ID NO: 02)
CAA75566 (SEQ ID NO: 31)
AAD34552 (SEQ ID NO: 32)
CAA75567 (SEQ ID NO: 33)
CAA76703 (SEQ ID NO: 34)
CAA57874 (SEQ ID NO: 35)
CAA91268 (SEQ ID NO: 36)

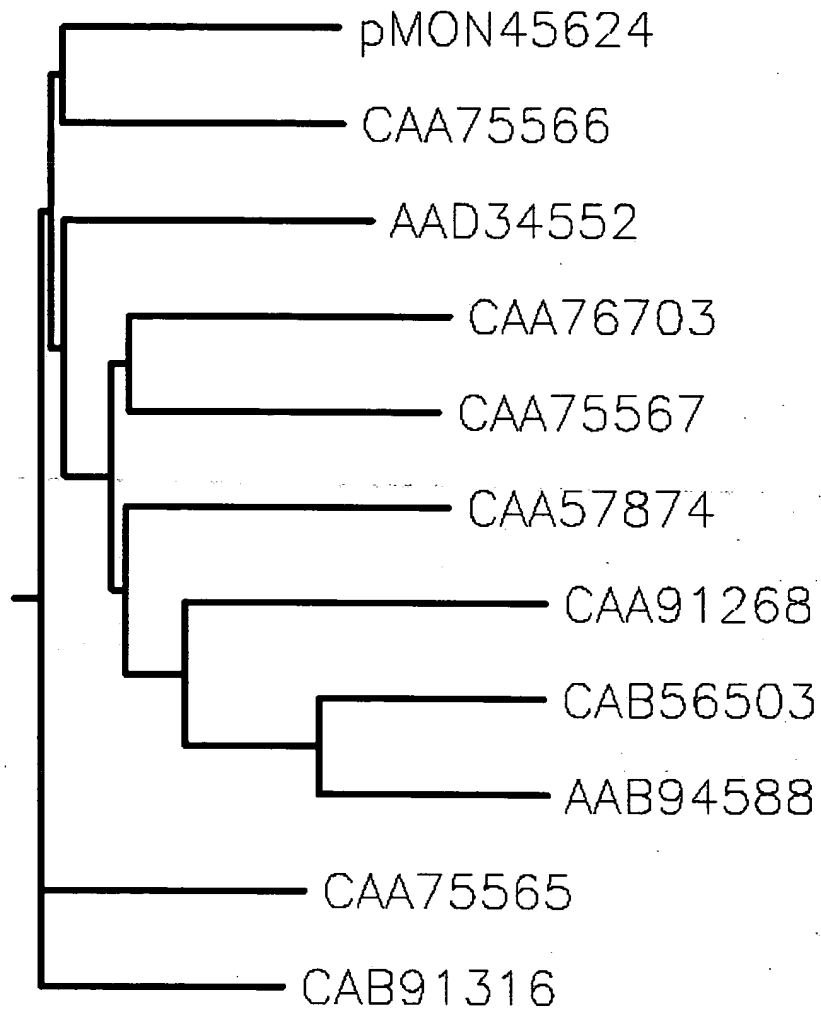
70 CAA75565 (SEQ ID NO: 27)
CAB91316 (SEQ ID NO: 28)
CAB56503 (SEQ ID NO: 29)
AAB94588 (SEQ ID NO: 30)
pMON45624 (SEQ ID NO: 02)
CAA75566 (SEQ ID NO: 31)
AAD34552 (SEQ ID NO: 32)
CAA75567 (SEQ ID NO: 33)
CAA76703 (SEQ ID NO: 34)
CAA57874 (SEQ ID NO: 35)
CAA91268 (SEQ ID NO: 36)

75 CAA75565 (SEQ ID NO: 27)
CAB91316 (SEQ ID NO: 28)
CAB56503 (SEQ ID NO: 29)
AAB94588 (SEQ ID NO: 30)
pMON45624 (SEQ ID NO: 02)
CAA75566 (SEQ ID NO: 31)
AAD34552 (SEQ ID NO: 32)
CAA75567 (SEQ ID NO: 33)
CAA76703 (SEQ ID NO: 34)
CAA57874 (SEQ ID NO: 35)
CAA91268 (SEQ ID NO: 36)

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**Figure 5 - Phylogenetic tree showing the relatedness of
Aspergillus ochraceus 11 alpha hydroxylase to the top 10
BLAST hits from GenBank**



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**Figure 6 – Percent homology of *Aspergillus ochraceus* 11
alpha hydroxylase to the top 10 BLAST hits from GenBank**

Accession Number	Species	% ID to 11a OH
CAB91316	<i>Neurospora crassa</i>	40
CAA76565	<i>Gibberella fujikuroi</i>	37
CAA75566	<i>Gibberella fujikuroi</i>	37
AAD34552	<i>Aspergillus terreus</i>	29
CAA75567	<i>Gibberella fujikuroi</i>	24
CAA57874	<i>Fusarium oxysporum</i>	24
CAA76703	<i>Gibberella fujikuroi</i>	23
CAB56503	<i>Catharanthus roseus</i>	14
AAB94588	<i>Glycine max</i>	14
CAA91268	<i>Caenorhabditis elegans</i>	12

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Figure 7 – Amino acid homology alignment of *A. ochraceus* and human oxidoreductase to NADPH cytochrome P450 reductases from *A. niger*, mouse, and *S. cerevisiae*

5	PMON45605	1	MGDSHMDTSSTVSEAVAEVSLFSMTDMILFSLIVGLTYWFLFRKKKEEMPEFTKIQTL
	human	1	MGDSHMDTSSTVSEAVAEVSLFSMTDMILFSLIVGLTYWFLFRKKKEEMPEFTKIQTL
	mouse	1	MGDSHMDTSATVPPRAVAEVSLESTTDIVLPSLIVGLTYWFLFRKKKEEMPEFTKIQTL
	PMON45632	1	--MQQDITLDLVLLVGLVGSVAYFTKG-----TYWAAADPYA--SAGPATGGG
	niger	1	--MQQDITLDLVLLVGLVGSVAYFTKG-----TYWAAADPYA--SAGPATGGG
10	yeast	1	--MPFGIDNDFTVLAGLVLAFLVLYKRN-----SIKELMSDDG-----DIT--
15	PMON45605	61	TSSVRESSEVEKMKRTGRNIIVFYGSQTGTAEFFANRLSKD-AHRYGMRGMSADPEEYDL
	human	61	TSSVRESSEVEKMKRTGRNIIVFYGSQTGTAEFFANRLSKD-AHRYGMRGMSADPEEYDL
	mouse	61	APPVKESSEVEKMKRTGRNIIVFYGSQTGTAEFFANRLSKD-AHRYGMRGMSADPEEYDL
	PMON45632	47	AKAGSTRDVIQKMDTGKNCVIFYGSQTGTAEVASRLAKEGSCRFGLTIVVADLEEYDY
	niger	47	AKAGSTRNIEKMEPTGKNCVIFYGSQTGTAEVASRLAKEGSCRFGLTIVVADLEEYDY
	yeast	42	AVSSGNRDIAVVTENNKNYLVLYASQTGTAEVAKKFSKELVAKFNLVNMCADVENYDF
20	PMON45605	120	ADLSSLPEIDNALVVFCMATYGECDPTDNACDFYDWLQ-----ET-----DVDLSGVKF
	human	120	ADLSSLPEIDNALVVFCMATYGECDPTDNACDFYDWLQ-----ET-----DVDLSGVKF
	mouse	120	ADLSSLPEIDNSLVVFCMATYGECDPTDNACDFYDWLQ-----ET-----DVDLTGVKF
	PMON45632	107	ENLEKFPB--DK--VAFEVUATYGECEPTDNAVEFYQFVTGDDAFAESGATADKELSSSKY
25	niger	107	ENLDQFPB--DK--VAFEVUATYGECEPTDNAVEFYQFVTGDDVAFES--ASADEKELSKY
	yeast	102	ESLNDVFPV----VVSIFISTYGECEFPFGAVNPEDFICN-----ABAG-----ALSNLR
30	PMON45605	169	AVFGLGNKTYEHFNAMGKYVDKRLEQLGAORIFELGLGDD--DGNLEEDFTTWREQFWPAV
	human	169	AVFGLGNKTYEHFNAMGKYVDKRLEQLGAORIFELGLGDD--DGNLEEDFTTWREQFWPAV
	mouse	169	AVFGLGNKTYEHFNAMGKYVDQRLEQLGAORIFELGLGDD--DGNLEEDFTTWREQFWPAV
	PMON45632	165	VTFGLGNNTYEHFNAMVENVDAALTKFGAQRIGSAGCGDDGACTMEEDFLAWKEPMAAAL
	niger	164	VAFGLGNNTYEHFNAMVRCVLAAPFKLGFQRIGSAGCGDDGACTMEEDFLAWKEPMAAAL
	yeast	148	NMFGLGNSTYEFENCAAKKAKEHL--SAAGAIRIRGLGSEDDGACTTDEDYNAKESILEVL
35	PMON45605	228	CBHFGMEATGEESSIROVELVHTL-----TDAARVYMGEVGRRLSY-----BNQNP
	human	228	CBHFGMEATGEESSIROVELVHTL-----TDAARVYMGEVGRRLSY-----BNQNP
	mouse	228	CBHFGMEATGEESSIROVELVHTL-----TDAARVYMGEVGRRLSY-----BNQNP
	PMON45632	225	SBAMNLA---ERDAVYEPVFNVTESLSPEDEMAYLGEPTQGHILQ-----GEFPG
40	niger	224	SBMDLE---ERDAVYEPVFNVTESLSPEDEMAYLGEPTQGHILQ-----GEFPG
	yeast	208	KIELHL---EAEAKFTSQFQYTVLN---EITDSGLGEPSAHYLPQHNLNRNADGICLG
45	PMON45605	275	PFDAKNPFLAAVTINRKUNOQTERHLMHLELDISDSKIRYESGDHVAVVPANDSALVNQL
	human	275	PFDAKNPFLAAVTINRKUNOQTERHLMHLELDISDSKIRYESGDHVAVVPANDSALVNQL
	mouse	275	PFDAKNPFLAAVTINRKUNOQTERHLMHLELDISDSKIRYESGDHVAVVPANDSTLVNQL
	PMON45632	273	PESAANPFLAFTSESRELFNVKDRNCUHMETSISAGSNFTYTGDDHIAVVPINAGSEVTRF
	niger	272	PESAANPFLAFTSESRELFNVKDRNCUHMETSISAGSNFTYTGDDHIAVVPINAGSEVTRF
50	yeast	262	PEDLSQPYIAFTVKSRELFSSNDNRCUHMETSISAGSNFTYTGDDHIAVVPINAGSEVTRF
55	PMON45605	335	GKILCAD--LDVMSLNNLDEESNKKHPFQPTSYRTALTYYLDITNFPRTNVLVELAQY
	human	335	GKILCAD--LDVMSLNNLDEESNKKHPFQPTSYRTALTYYLDITNFPRTNVLVELAQY
	mouse	335	GEILCAD--LDVMSLNNLDEESNKKHPFQPTSYRTALTYYLDITNFPRTNVLVELAQY
	PMON45632	333	LQAFGLEGRHSVINIKGID--VTAKVEITPTTYDAARVYLEVCAVSRQFVSTLAAF
	niger	332	LQAFGLEGRHSVINIKGID--VTAKVEITPTTYDAARVYLEVCAVSRQFVSTLAAF
	yeast	322	LSIFNLQ--PETTFDKELD--PTVVPFPTETTIGAAKKHYLEITCFVSRQFSSLIQF
60	PMON45605	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDQF--SLRFPIDHLCCELLPR
	human	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDQF--SLRFPIDHLCCELLPR
	mouse	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDQF--SLRFPIDHLCCELLPR
	PMON45632	391	APDEATKAEIVHLGDKDYFHEKHTNRCFNIAQ--ALQSHTSKE--FSAVFSLIEGCTIF
65	niger	390	APMRKARQRCVWVAQG-LFHEGHQPMQHAQ--ALQSHTSKE--FSAVFSLIEGCTIF
	yeast	378	APNADVKEKLTLLSKDKDQFVETTSKFNIAQ--ALKYLSGAKWDNVNPOFVSESVEQ
70	PMON45605	451	LQARYYSTASSSKVHPNSVHICAVVVEYETK---AGRINKGVATNWLRAKEF--AGE--
	human	451	LQARYYSTASSSKVHPNSVHICAVVVEYETK---AGRINKGVATNWLRAKEF--AGE--
	mouse	451	LQARYYSTASSSKVHPNSVHICAVVEYEAQ---SCRINKGVATNWLRAKEF--AGE--
	PMON45632	448	LQFRYYSTSSSLVQKKKISTAVVESVRLP---GEBHIVRGVITNLLALKKQKNGECS
	niger	446	LQFRYYSTSSSLVQKKKISTAVVESVRLP---GASHIVRGVITNLLALKKQKNGRSL
	yeast	436	YTFRYYSTSSSLSEKQTVHVTSTVEN--PNPELP--DAPPGVGVITNLLRNILACNNVNI

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← insert

"Figure 7, continued"

5 PMON45605 503 -----NCGF-----ALVPHFVRKKSQFRLPFRATTTPVIMVGPCTGVAPFIFGFIQE
human 503 -----NCGF-----ALVPHFVRKKSQFRLPFRATTTPVIMVGPCTGVAPFIFGFIQE
mouse 503 -----NCGF-----ALVPHFVRKKSQFRLPFRATTTPVIMVGPCTGVAPFIFGFIQE
pMON45632 505 PDPHG-LTYSITGPRNKIDGIVPMHVRHSNFKLPSPDSRFVIMVGPCTGVAPFRGFIE
niger 503 SRPSR-LDLLHGGPRNKIDGIVPMHVRHSNFKLPSPDSRFVIMVGPCTGVAPFRGFIE
yeast 495 AETNLFVHYDLNCPKLEANYKLPFHVFRSNFRLPSPDSRFVIMVGPCTGVAPFRGFIRE

10 PMON45605 547 RAWLRQ---QGKE---VGETLLYGCRRSDEDLYREELACFHRD-GALTQLNVAFSRE-
human 547 RAWLRQ---QGKE---VGETLLYGCRRSDEDLYREELACFHRD-GALTQLNVAFSRE-
mouse 547 RAWLRQ---QGKE---VGETLLYGCRRSDEDLYREELARFHKD-GALTQLNVAFSRE-
pMON45632 564 RAALAA---KGEK---VGTTLFFGCRFSDEDFLYKDEWKTFOQLCDSLKIITAFSRE-
niger 562 RAALAA---KGEK---VGTTLFFGCRFSDEDFLYKDEWKTIVQDQLCDNLKIITAFSRE-
yeast 555 RVAFLESQKKGNNVSLCKHLELYGSRNID-DFLYQDEWPEYAKKLDGSHEMVAHSRLP

15 PMON45605 599 QSHKVYVOHLLKQDREHLWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMAHAC
human 599 QSHKVYVOHLLKQDREHLWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMAHAC
mouse 599 QSHKVYVOHLLKQDREHLWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMAHAC
pMON45632 617 SAEKVYVOHLLKQDREHLWKLI-EGGAHIYVCGDARNMAREVNLVLGQITAKQRCIPADK
niger 615 GPKKVYVOHLLKQDREHLWKLI-EGGAHIYVCGDARNMAREVNLVLGQITAKQRCIPADK
yeast 614 NTKKVYVOHLLKQDREHLWKLI-EGGAHIYVCGDARNMAREVNLVLGQITAKQRCIPADK

20 PMON45605 658 AVDYTKKLMTRGRYSLDVWS
human 658 AVDYTKKLMTRGRYSLDVWS
mouse 659 AVDYTKKLMTRGRYSLDVWS
pMON45632 676 GBEWVKKHMRSSGYSQDDVWS
niger 674 GBEWVKKHMRSSGYSQDDVWS
yeast 673 ATELEMKLTSGRYSQDDVWS

25 PMON45605 (SEQ ID NO: 03)
human (SEQ ID NO: 06)
mouse (SEQ ID NO: 39)
pMON45632 (SEQ ID NO: 05)
niger (SEQ ID NO: 38)
yeast (SEQ ID NO: 37)

30 PMON45605 (SEQ ID NO: 03)
human (SEQ ID NO: 06)
mouse (SEQ ID NO: 39)
pMON45632 (SEQ ID NO: 05)
niger (SEQ ID NO: 38)
yeast (SEQ ID NO: 37)

35 PMON45605 (SEQ ID NO: 03)
human (SEQ ID NO: 06)
mouse (SEQ ID NO: 39)
pMON45632 (SEQ ID NO: 05)
niger (SEQ ID NO: 38)
yeast (SEQ ID NO: 37)

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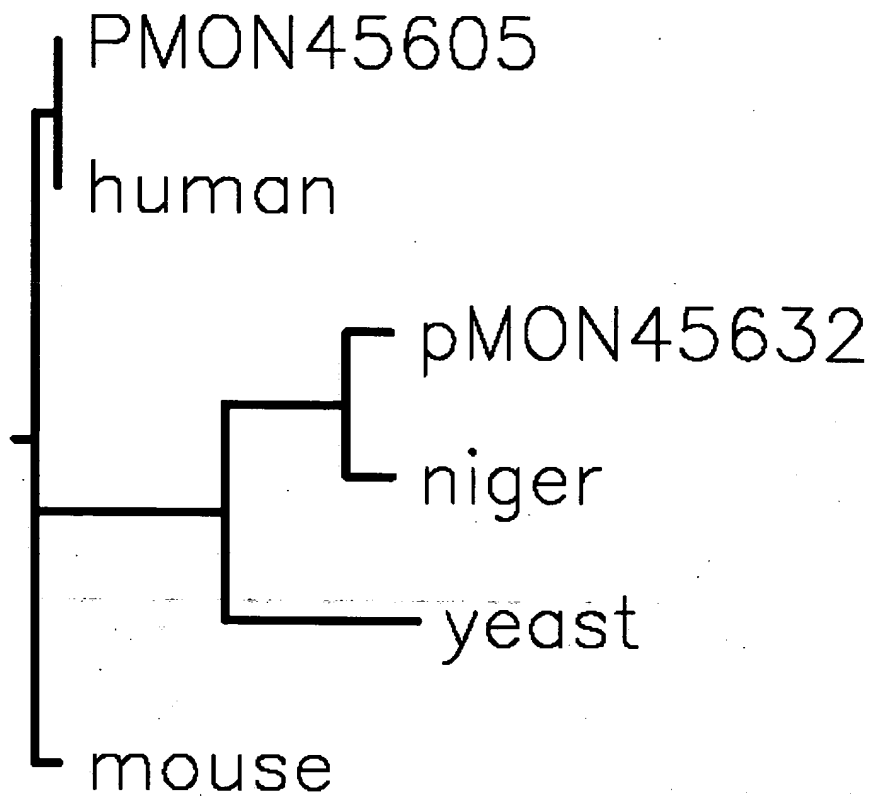
Figure 8 – Amino acid homology alignment of *A. ochraceus* oxidoreductase to NADPH cytochrome P450 reductases from *A. niger* and *S. cerevisiae*

5	A.niger	1	MAQLDTLDLVLLVLLVGSVAYFTKGTWAVAKTRMPLPARRNGAAKAGKTRNIEKM
	A.ochraceus	1	MAQLDTLDLVLLVLLVGSVAYFTKGTWAVAKTRMPLPARRNGAAKAGKTRDIOVM
	S.cerevisiae	1	MPFGEDNTDFTVLAGLAVLLVVKRNGSIKELLMSDDCDITAVSSC-----NRDHACVV
10	A.niger	60	ETGKNCVIFYGSQTGTAEDYASRLAKEGSORFGLKTMVADLEEYDYNLTQFPEDKVAE
	A.ochraceus	60	ETGKNCVIFYGSQTGTAEDYASRLAKEGSORFGLKTMVADLEEYDYNLTQFPEDKVAE
	S.cerevisiae	55	EDNNKNYLVLVYSQTGTAEDYAKKFSKELVAKENLNVMCADVENYDEESLNDVH--VIVS
15	A.niger	120	FVLATYGEGETPDNAVEFYQFTGDDVAFES-ASADKPLSKLYVAFGLGNNTYEHYNA
	A.ochraceus	120	FVLATYGEGETPDNAVEFYQFTGDDVAFES-ASADKPLSKLYVAFGLGNNTYEHYNA
	S.cerevisiae	113	IFISTYGEGETPDNAVEFYQFTGDDVAFES-ASADKPLSKLYVAFGLGNNTYEHYNA
20	A.niger	179	MVROVDAAFORLCPORIGSAGEGDDGACTMEEDFLAWKEPMWAALSSEMCLEEREAVYEE
	A.ochraceus	180	MVRNVDAALRRFGAORIGSAGEGDDGACTMEEDFLAWKEPMWAALSSEMCLEEREAVYEE
	S.cerevisiae	163	AAKKAEEKHLSAAGATFELCKLGEADDGAGTDEDTMAWKDSILEVLKREHLDECEAKFTS
25	A.niger	239	VECVTENESLSPEDETIVLGEPTQSHLC-----CTPKGPYSAHNPFIAPISRESRL
	A.ochraceus	240	VENVTEDESLSPEDETIVLGEPTQSHLC-----CTPKGPYSAHNPFIAPISRESRL
	S.cerevisiae	223	CEQYI---VINEITDSMSLGEPSAHYLPESHQLNRRNACIQLGPEPDLSCQPIAPIVRSRL
30	A.niger	290	ETVKDRNCLHMEISLAGSNLSYQTGDHIAVWPTNAGAEVDRFLQVFGLEGKRDSSVINIKG
	A.ochraceus	291	ETVKDRNCLHMEISLAGSNLSYQTGDHIAVWPTNAGAEVDRFLQVFGLEGKRDSSVINIKG
	S.cerevisiae	280	ESSNDRNCLHSEFDLGGSNIRYSQTGDHIAVWPTNAGAEVDRFLQVFGLEGKRDSSVINIKG
35	A.niger	350	IDVTAKVPIPTPTTYDAAVRYMEVCAVPSRQFVATLAFAFMKARORLCVWVAQG-LF
	A.ochraceus	351	IDVTAKVPIPTPTTYDAAVRYMEVCAVPSRQFVATLAFAFMKARORLCVWVAQG-LF
	S.cerevisiae	338	LEFTVKVEFPPTPTTGAAIRHYLETGPVSRQLFSSLIQFAFNADVREKLTLLSKDKDQF
40	A.niger	409	PREGHCPMLCHAAQLOSITS-KPFSAVPFSLLEIGITKLOPRYYSISSSSLVQDKISIT
	A.ochraceus	411	HEKITNECFENIAQALQSITS-KPFSAVPFSLLEIGITKLOPRYYSISSSSLVQDKISIT
	S.cerevisiae	398	AVEITISKYFNIAADALKYLSGAKLDNVFMQFLVESYPMIPRYYSISSSSLSSENQTVHVT
45	A.niger	468	AVVESVRLP---CASHMVKGVTTNYLLALNOKNCRSLSRFSR-IDLLHGGPRNKYDGIHV
	A.ochraceus	470	AVVESVRLP---CASHMVKGVTTNYLLALNOKNCRSLSRFSR-IDLLHGGPRNKYDGIHV
	S.cerevisiae	458	STVENFPNLELEFDAPPVGVTNMLRNHQLAONNVNIAETNLPVHYDINGPRKLEANYKL
50	A.niger	525	PVHVRHSNFKLPSPDSRPFIMVGPGTGVAPFRGFIQERAAALAAKGER-----VGPITVLF
	A.ochraceus	527	PVHVRHSNFKLPSPDSRPFIMVGPGTGVAPFRGFIQERAAALAAKGER-----VGPITVLF
	S.cerevisiae	518	PVHVRHSNFKLPSPDSRPFIMVGPGTGVAPFRGFIQERAAALAAKGER-----VGPITVLF
	A.niger	579	FGCRKSDDEFLYKDEWKTFOEQLGDSLKIIITAFSRE-GPKVYVQHRLREHSELVSDLLK
	A.ochraceus	581	FGCRKSDDEFLYKDEWKTFOEQLGDSLKIIITAFSRE-SABKVYVQHRLREHSELVSDLLK
	S.cerevisiae	578	YCSRNTD--DFLYQDEMPYAKKLDGSFEMVAHSRLPNTKKVYVQDRLKYEHCQFEMIN
	A.niger	638	QKATFYVCGDAANMAREVNLVLGQIIAQRGLPAEKGEEMVKHMRRCRYQEDVWS
	A.ochraceus	640	QKATFYVCGDAANMAREVNLVLGQIIAQRGLPAEKGEEMVKHMRRCRYQEDVWS
	S.cerevisiae	637	NCATFYVCGDAKGMANGVSTALVGLSRGKSITTEATELLHMLKTSGRYQEDVW-
	A.ochraceus, PMON45632	(SEQ ID NO: 05)	
	A.niger	(SEQ ID NO: 38)	
	S.cerevisiae, yeast	(SEQ ID NO: 37)	

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Figure 9 – Phylogenetic tree showing the relatedness of *Aspergillus ochraceus* and human oxidoreductase to reductases from *A. niger*, yeast, and mouse.



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Figure 10 – Percent homology between *Aspergillus ochraceus* oxidoreductase to reductases from *A. niger*, yeast, and mouse and human.

Accession number	organism	% id to A.och oxred
CAA81550	<i>A. niger</i>	84
BAA02936	<i>S. cerevisiae</i>	37
BAA04496	mouse	34
AAB21814	human	33

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Figure 11 – Amino acid homology alignment of human oxidoreductase with the top 4 hits from SwissProt

5	PMON45605	1	MGDSHVDTSSTVSEAVAEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEEVPEFTKIQT
	human	1	MGDSHVDTSSTVSEAVAEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEEVPEFTKIQT
	rabbit	1	MADSHGDTGATPEAAQEAQSMFSMTDMVLFSIVGLLTYWFLFRKKKEEVPEFTKIQAP
	rat	1	MGDSHEDTSATVSEAVAEVSLFSMTDMVLFSIVGLTYWFLFRKKKEETPEFSKIQT
	mouse	1	MGDSHEDTSATVSEAVAEVSLFSMTDIVLFSIVGLTYWFLFRKKKEETPEFSKIQT
10	pig	1	MGDSNVDTGTITSEAVAEVSLFSMTDMVLFSIVGLLTYWFLFRKKKDEVPEFSKIET
15	PMON45605	61	TSS-VRESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	human	61	TSS-VRESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	rabbit	61	TSS-VKESFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMAADPEEYDL
	rat	61	APP-VKESFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	mouse	61	APP-VKESFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	pig	61	TSS-VKSSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMAADPEEYDL
20	PMON45605	120	ADLSSLPEIDNALVFCMATYGECDPTDNAQDFYDWLQETDVLGKFAVFLGNKTYE
	human	120	ADLSSLPEIDNALVFCMATYGECDPTDNAQDFYDWLQETDVLGKFAVFLGNKTYE
	rabbit	121	ADLSSLPEIDNALVFCMATYGECDPTDNAQDFYDWLQETDVLGKFAVFLGNKTYE
	rat	120	ADLSSLPEIDKSLVFCMATYGECDPTDNAQDFYDWLQETDVLGKFAVFLGNKTYE
	mouse	120	ADLSSLPEIDKSLVFCMATYGECDPTDNAQDFYDWLQETDVLGKFAVFLGNKTYE
25	pig	120	ADLSSLPEIDNALVFCMATYGECDPTDNAQDFYDWLQETDVLGKFAVFLGNKTYE
30	PMON45605	180	HFNAMGKYVDKRLQOLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
	human	180	HFNAMGKYVDKRLQOLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
	rabbit	181	HFNAMGKYVDKRLQOLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
	rat	180	HFNAMGKYVDKRLQOLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
	mouse	180	HFNAMGKYVDKRLQOLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
	pig	180	HFNAMGKYVDKRLQOLGAQRIFDLGLGDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
35	PMON45605	240	SSIRQYELVVHTDITLAAKVYMGEMGRKLSYENQKPPDAKNPFLAAVTTNRKLNQGTERH
	human	240	SSIRQYELVVHTDITLAAKVYMGEMGRKLSYENQKPPDAKNPFLAAVTTNRKLNQGTERH
	rabbit	241	SSIRQYELVHTDITLAAKVYMGEMGRKLSYENQKPPDAKNPFLAAVTTNRKLNQGTERH
	rat	240	SSIRQYELVVHTDITLAAKVYMGEMGRKLSYENQKPPDAKNPFLAAVTTNRKLNQGTERH
40	mouse	240	SSIRQYELVVHTDITLAAKVYMGEMGRKLSYENQKPPDAKNPFLAAVTTNRKLNQGTERH
	pig	240	SSIRQYELVVHTDITLAAKVYMGEMGRKLSYENQKPPDAKNPFLAAVTTNRKLNQGTERH
45	PMON45605	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGTEILGADLDVVMISLNNLDEESNKKH
	human	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGTEILGADLDVVMISLNNLDEESNKKH
	rabbit	301	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGTEILGADLDVVMISLNNLDEESNKKH
	rat	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGTEILGADLDVVMISLNNLDEESNKKH
	mouse	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGTEILGADLDVVMISLNNLDEESNKKH
50	pig	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGTEILGADLDVVMISLNNLDEESNKKH
	PMON45605	360	PFPCPTSYRTALTYLDITNPRTNVLYELAQYASEPSEQELRRKMSSSGEGKELYLSW

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"figure 11, continued"

5 human 360 PFPCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQEHLRKMASSSGEGKELYLSW
rabbit 361 PFPCPTSYRTALTYLDITNPPRTNVLYELAQYADPAEQEHLRKMASSSGEGKELYLSW
rat 360 PFPCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQEHLRKMASSSGEGKELYLSW
mouse 360 PFPCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQEHLRKMASSSGEGKELYLSW
pig 360 PFPCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQEHLRKMASSSGEGKELYLSW

10 PMON45605 420 VVEARRHILAILQDCPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVEYE
human 420 VVEARRHILAILQDCPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVEYE
rabbit 421 VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVEYE
rat 420 VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVEYE
mouse 420 VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVEYE
pig 420 VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVEYE

15 PMON45605 480 TRAGRINKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAE
human 480 TRAGRINKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAE
rabbit 481 TRAGRINKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAE
rat 480 ATRGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAE
20 mouse 480 ATRGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAE
pig 480 TRSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAE

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"Figure 11, continued"

5

PMON45605 540 FIGFIQERAWLRQGGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGAQTQNLNVAFSREQ
human 540 FIGFIQERAWLRQGGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGAQTQNLNVAFSREQ
rabbit 541 FIGFIQERAWLRQGGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGAQTQNLNVAFSREQ
rat 540 FIGFIQERAWLRQGGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGAQTQNLNVAFSREQ
mouse 540 FIGFIQERAWLRQGGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGAQTQNLNVAFSREQ
pig 540 FIGFIQERAWLRQGGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGAQTQNLNVAFSREQ

10

PMON45605 600 SHKVYVQHLLKQDREHLWKLIEGGAHYVCGDARNMARDVQNTFYDIVAELGMEHAQA
human 600 SHKVYVQHLLKQDREHLWKLIEGGAHYVCGDARNMARDVQNTFYDIVAELGMEHAQA
rabbit 601 SHKVYVQHLLKRDKEHLWKLIEGGAHYVCGDARNMARDVQNTFYDIVAELGMEHAQA
rat 600 SHKVYVQHLLKRDKEHLWKLIEGGAHYVCGDARNMARDVQNTFYDIVAELGMEHAQA
mouse 600 SHKVYVQHLLKRDKEHLWKLIEGGAHYVCGDARNMARDVQNTFYDIVAELGMEHAQA
pig 600 SHKVYVQHLLKRDKEHLWKLIEGGAHYVCGDARNMARDVQNTFYDIVAELGMEHAQA

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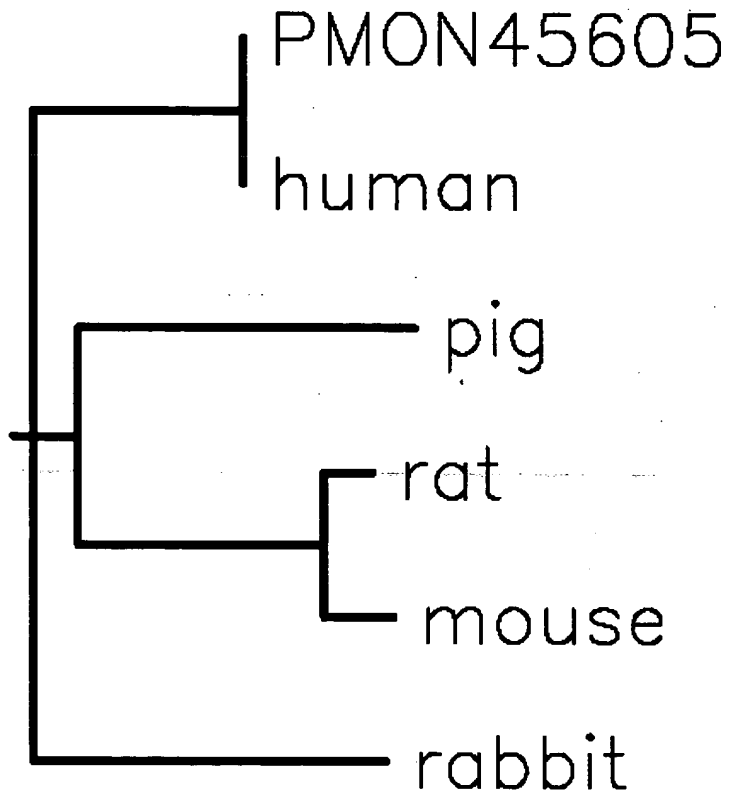
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PMON45605 659 VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 03)
human 659 VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 52)
rabbit 661 VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 53)
rat 660 VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 54)
mouse 660 VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 55)
pig 660 VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 56)

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**Figure 12 – Phylogenetic tree showing the relatedness of
human oxidoreductase (P16435) with top 4 hits from
SwissProt**



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**Figure 13 – Percent homology between human oxidoreductase
and top 4 hits from SwissProt**

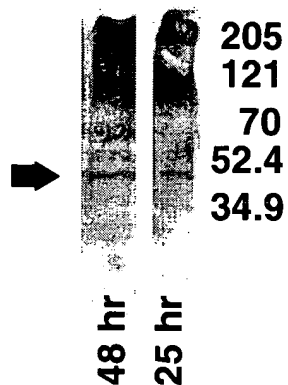
Accession number	Species	% id to human oxred
P00388	rat	92
P00389	rabbit	92
P37040	mouse	92
P04175	pig	91

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Figure 14 - Expression of *Aspergillus ochraceus* 11 alpha hydroxylase in transfected Sf9 insect cells

Expression of 11- α -Hydroxylase in Transfected Sf9 Cells

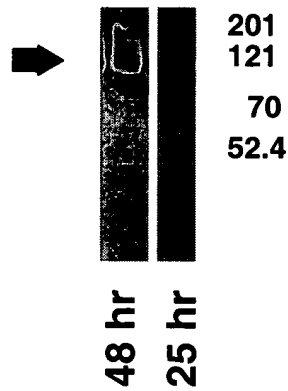


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**Figure 15 - Expression of *Aspergillus ochraceus* P450
oxidoreductase in transfected Sf9 insect cells**

**Expression of Fungal P-450 Oxidoreductase
in Transfected Sf9 Cells**



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Figure 16 - Conversion of androstenedione to 11 alpha hydroxy androstenedione monitored by HPLC

